

SEQUENCE LISTING

<110> The Genetics Company

<120> Growth Regulating Proteins

<130> 06259PC

<160> 5

<170> PatentIn version 3.1

<210> 1

<211> 2096

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76)..(1950)

<223>

<400> 1

ggcacgaggc ggaagtgttc cggggtccgt ggggagcagg agagggaggc ggcggaccgt 60

cccgcgcggg gcacg atg ttg aac atg tgg aag gtg cgc gag ctg gtg gac 111
 Met Leu Asn Met Trp Lys Val Arg Glu Leu Val Asp
 1 5 10

aaa gcc acc aat gtt gtt atg aat tat tca gag atc gag tct aag gtt 159
 Lys Ala Thr Asn Val Val Met Asn Tyr Ser Glu Ile Glu Ser Lys Val

15

20

25

cga gag gca acg aac gat gat cct tgg gga cct tct ggg caa ctc atg 207

Arg	Glu	Ala	Thr	Asn	Asp	Asp	Pro	Trp	Gly	Pro	Ser	Gly	Gln	Leu	Met		
30						35					40						
gga	gag	att	gcc	aag	gct	aca	ttt	atg	tat	gaa	caa	ttt	cca	gaa	ctt	255	
Gly	Glu	Ile	Ala	Lys	Ala	Thr	Phe	Met	Tyr	Glu	Gln	Phe	Pro	Glu	Leu		
45					50					55					60		
atg	aac	atg	ctt	tgg	tca	cga	atg	tta	aaa	gac	aac	aaa	aag	aat	tgg	303	
Met	Asn	Met	Leu	Trp	Ser	Arg	Met	Leu	Lys	Asp	Asn	Lys	Lys	Asn	Trp		
				65					70						75		
aga	aga	gtt	tat	aag	tcg	ttg	ctg	ctc	cta	gct	tac	ctc	ata	agg	aat	351	
Arg	Arg	Val	Tyr	Lys	Ser	Leu	Leu	Leu	Leu	Ala	Tyr	Leu	Ile	Arg	Asn		
			80						85					90			
gga	tca	gag	cgt	gtt	gtt	aca	agt	gcc	aga	gaa	cac	att	tat	gat	tta	399	
Gly	Ser	Glu	Arg	Val	Val	Thr	Ser	Ala	Arg	Glu	His	Ile	Tyr	Asp	Leu		
		95					100					105					
cga	tcc	ctg	gaa	aat	tac	cac	ttt	gta	gat	gag	cat	ggg	aag	gat	caa	447	
Arg	Ser	Leu	Glu	Asn	Tyr	His	Phe	Val	Asp	Glu	His	Gly	Lys	Asp	Gln		
	110					115						120					
ggg	ata	aat	att	cga	cag	aag	gtg	aag	gaa	ttg	gtt	gaa	ttt	gcc	cag	495	
Gly	Ile	Asn	Ile	Arg	Gln	Lys	Val	Lys	Glu	Leu	Val	Glu	Phe	Ala	Gln		
125					130					135					140		
gat	gac	gac	agg	ctt	cgt	gaa	gag	cga	aag	aaa	gca	aag	aag	aac	aaa	543	
Asp	Asp	Asp	Arg	Leu	Arg	Glu	Glu	Arg	Lys	Lys	Ala	Lys	Lys	Asn	Lys		
				145					150						155		
gac	aag	tat	gtt	ggg	gtt	tcc	tca	gac	agt	gtt	gga	gga	ttc	aga	tac	591	
Asp	Lys	Tyr	Val	Gly	Val	Ser	Ser	Asp	Ser	Val	Gly	Gly	Phe	Arg	Tyr		
			160					165					170				
agt	gaa	aga	tat	gat	cct	gag	ccc	aaa	tca	aaa	tgg	gat	gag	gag	tgg	639	
Ser	Glu	Arg	Tyr	Asp	Pro	Glu	Pro	Lys	Ser	Lys	Trp	Asp	Glu	Glu	Trp		
		175					180					185					
gat	aaa	aac	aag	agt	gct	ttt	cca	ttc	agt	gat	aaa	tta	ggg	gag	ctg	687	
Asp	Lys	Asn	Lys	Ser	Ala	Phe	Pro	Phe	Ser	Asp	Lys	Leu	Gly	Glu	Leu		
	190					195					200						
agt	gat	aaa	att	gga	agc	aca	att	gat	gac	acc	atc	agc	aag	ttc	cgg	735	
Ser	Asp	Lys	Ile	Gly	Ser	Thr	Ile	Asp	Asp	Thr	Ile	Ser	Lys	Phe	Arg		
205					210					215					220		
agg	aaa	gat	aga	gaa	gac	tct	cca	gaa	aga	tgc	agc	gac	agc	gat	gag	783	
Arg	Lys	Asp	Arg	Glu	Asp	Ser	Pro	Glu	Arg	Cys	Ser	Asp	Ser	Asp	Glu		
				225					230					235			
gaa	aag	aaa	gcg	aga	aga	ggc	aga	tct	ccc	aaa	ggg	gaa	ttc	aaa	gat	831	
Glu	Lys	Lys	Ala	Arg	Arg	Gly	Arg	Ser	Pro	Lys	Gly	Glu	Phe	Lys	Asp		
			240					245					250				
gaa	gag	gag	act	gtg	acg	aca	aag	cat	att	cat	atc	aca	cag	gcc	aca	879	

Glu	Glu	Glu	Thr	Val	Thr	Thr	Lys	His	Ile	His	Ile	Thr	Gln	Ala	Thr		
		255					260					265					
gag	acc	acc	aca	acc	aga	cac	aag	cgc	aca	gca	aat	cct	tcc	aaa	acc	927	
Glu	Thr	Thr	Thr	Thr	Arg	His	Lys	Arg	Thr	Ala	Asn	Pro	Ser	Lys	Thr		
		270					275					280					
att	gat	ctt	gga	gca	gca	gca	cat	tac	aca	ggg	gac	aaa	gca	agt	cca	975	
Ile	Asp	Leu	Gly	Ala	Ala	Ala	His	Tyr	Thr	Gly	Asp	Lys	Ala	Ser	Pro		
285					290					295					300		
gat	cag	aat	gct	tca	acc	cac	aca	cct	cag	tct	tca	ggt	aag	act	tca	1023	
Asp	Gln	Asn	Ala	Ser	Thr	His	Thr	Pro	Gln	Ser	Ser	Val	Lys	Thr	Ser		
			305						310					315			
gtg	cct	agc	agc	aag	tca	tct	ggg	gac	ctt	ggt	gat	ctg	ttt	gat	ggc	1071	
Val	Pro	Ser	Ser	Lys	Ser	Ser	Gly	Asp	Leu	Val	Asp	Leu	Phe	Asp	Gly		
		320						325					330				
acc	agc	cag	tca	aca	gga	gga	tca	gct	gat	tta	ttc	gga	gga	ttt	gct	1119	
Thr	Ser	Gln	Ser	Thr	Gly	Gly	Ser	Ala	Asp	Leu	Phe	Gly	Gly	Phe	Ala		
		335					340					345					
gac	ttt	ggc	tca	gct	gct	gca	tca	ggc	agt	ttc	cct	tcc	caa	gta	aca	1167	
Asp	Phe	Gly	Ser	Ala	Ala	Ala	Ser	Gly	Ser	Phe	Pro	Ser	Gln	Val	Thr		
	350					355					360						
gca	aca	agt	ggg	aat	gga	gac	ttt	ggg	gac	tgg	agt	gcc	ttc	aac	caa	1215	
Ala	Thr	Ser	Gly	Asn	Gly	Asp	Phe	Gly	Asp	Trp	Ser	Ala	Phe	Asn	Gln		
365					370				375						380		
gcc	cca	tca	ggc	cct	ggt	gct	tcc	agt	ggc	gag	ttc	ttt	ggc	agt	gcc	1263	
Ala	Pro	Ser	Gly	Pro	Val	Ala	Ser	Ser	Gly	Glu	Phe	Phe	Gly	Ser	Ala		
				385					390					395			
tca	cag	cca	gcg	gta	gaa	ctt	ggt	agt	ggc	tca	caa	tca	gct	cta	ggc	1311	
Ser	Gln	Pro	Ala	Val	Glu	Leu	Val	Ser	Gly	Ser	Gln	Ser	Ala	Leu	Gly		
			400						405				410				
cca	cct	cct	gct	gcc	tca	aat	tct	tca	gac	ctg	ttt	gat	ctt	atg	ggc	1359	
Pro	Pro	Pro	Ala	Ala	Ser	Asn	Ser	Ser	Asp	Leu	Phe	Asp	Leu	Met	Gly		
		415					420					425					
tcg	tcc	cag	gca	acc	atg	aca	tct	tcc	cag	agt	atg	aat	ttc	tct	atg	1407	
Ser	Ser	Gln	Ala	Thr	Met	Thr	Ser	Ser	Gln	Ser	Met	Asn	Phe	Ser	Met		
	430					435					440						
atg	agc	act	aac	act	gtg	gga	ctt	ggg	ttg	cct	atg	tca	aga	tca	cag	1455	
Met	Ser	Thr	Asn	Thr	Val	Gly	Leu	Gly	Leu	Pro	Met	Ser	Arg	Ser	Gln		
445					450				455						460		
aat	aca	gat	atg	gtc	cag	aaa	tca	gtc	agc	aaa	acc	ttg	ccc	tct	act	1503	
Asn	Thr	Asp	Met	Val	Gln	Lys	Ser	Val	Ser	Lys	Thr	Leu	Pro	Ser	Thr		
				465					470					475			

tgg tct gac ccc agt gta aac atc agc cta gac aac tta cta cct ggt	1551
Trp Ser Asp Pro Ser Val Asn Ile Ser Leu Asp Asn Leu Leu Pro Gly	
480 485 490	
atg cag cct tcc aaa ccc cag cag cca tca ctg aat aca atg att cag	1599
Met Gln Pro Ser Lys Pro Gln Gln Pro Ser Leu Asn Thr Met Ile Gln	
495 500 505	
caa cag aat atg cag cag cct atg aat gtg atg act caa agt ttt gga	1647
Gln Gln Asn Met Gln Gln Pro Met Asn Val Met Thr Gln Ser Phe Gly	
510 515 520	
gct gtg aac ctc agt tct cca tcg aac atg ctt cct gtc cgg ccc caa	1695
Ala Val Asn Leu Ser Ser Pro Ser Asn Met Leu Pro Val Arg Pro Gln	
525 530 535 540	
act aat gct ttg ata ggg gga ccc atg cct atg agc atg ccc aat gtg	1743
Thr Asn Ala Leu Ile Gly Gly Pro Met Pro Met Ser Met Pro Asn Val	
545 550 555	
atg act ggc acc atg gga atg gcc cct ctt gga aat act ccg atg atg	1791
Met Thr Gly Thr Met Gly Met Ala Pro Leu Gly Asn Thr Pro Met Met	
560 565 570	
aac cag agc atg atg ggc atg aac atg aac ata ggg atg tcc gct gct	1839
Asn Gln Ser Met Met Gly Met Asn Met Asn Ile Gly Met Ser Ala Ala	
575 580 585	
ggg atg ggc ttg aca ggc aca atg gga atg ggc atg ccc aac ata gcc	1887
Gly Met Gly Leu Thr Gly Thr Met Gly Met Gly Met Pro Asn Ile Ala	
590 595 600	
atg act tct gga act gtg caa ccc aag caa gat gcc ttt gca aat ttc	1935
Met Thr Ser Gly Thr Val Gln Pro Lys Gln Asp Ala Phe Ala Asn Phe	
605 610 615 620	
gcc aat ttt agc aaa taagagattg taaaagaagc agattgaatg aagaattttt	1990
Ala Asn Phe Ser Lys	
625	
agctgtgcag ataggtgatg ttgggatgga aaatgctaata caactaccct ttcttttatac	2050
aagtaattaa aataaatcta cataaaaaaaaa aaaaaaaaaa aaaaaa	2096

<210> 2

<211> 625

<212> PRT

<213> Homo sapiens

<400> 2

Met Leu Asn Met Trp Lys Val Arg Glu Leu Val Asp Lys Ala Thr Asn
1 5 10 15

Val Val Met Asn Tyr Ser Glu Ile Glu Ser Lys Val Arg Glu Ala Thr
20 25 30

Asn Asp Asp Pro Trp Gly Pro Ser Gly Gln Leu Met Gly Glu Ile Ala
35 40 45

Lys Ala Thr Phe Met Tyr Glu Gln Phe Pro Glu Leu Met Asn Met Leu
50 55 60

Trp Ser Arg Met Leu Lys Asp Asn Lys Lys Asn Trp Arg Arg Val Tyr
65 70 75 80

Lys Ser Leu Leu Leu Leu Ala Tyr Leu Ile Arg Asn Gly Ser Glu Arg
85 90 95

Val Val Thr Ser Ala Arg Glu His Ile Tyr Asp Leu Arg Ser Leu Glu
100 105 110

Asn Tyr His Phe Val Asp Glu His Gly Lys Asp Gln Gly Ile Asn Ile
115 120 125

Arg Gln Lys Val Lys Glu Leu Val Glu Phe Ala Gln Asp Asp Asp Arg
130 135 140

Leu Arg Glu Glu Arg Lys Lys Ala Lys Lys Asn Lys Asp Lys Tyr Val
145 150 155 160

Gly Val Ser Ser Asp Ser Val Gly Gly Phe Arg Tyr Ser Glu Arg Tyr
165 170 175

Asp Pro Glu Pro Lys Ser Lys Trp Asp Glu Glu Trp Asp Lys Asn Lys
180 185 190

Ser Ala Phe Pro Phe Ser Asp Lys Leu Gly Glu Leu Ser Asp Lys Ile
195 200 205

Gly Ser Thr Ile Asp Asp Thr Ile Ser Lys Phe Arg Arg Lys Asp Arg
210 215 220

Glu Asp Ser Pro Glu Arg Cys Ser Asp Ser Asp Glu Glu Lys Lys Ala
 225 230 235 240

Arg Arg Gly Arg Ser Pro Lys Gly Glu Phe Lys Asp Glu Glu Glu Thr
 245 250 255

Val Thr Thr Lys His Ile His Ile Thr Gln Ala Thr Glu Thr Thr Thr
 260 265 270

Thr Arg His Lys Arg Thr Ala Asn Pro Ser Lys Thr Ile Asp Leu Gly
 275 280 285

Ala Ala Ala His Tyr Thr Gly Asp Lys Ala Ser Pro Asp Gln Asn Ala
 290 295 300

Ser Thr His Thr Pro Gln Ser Ser Val Lys Thr Ser Val Pro Ser Ser
 305 310 315 320

Lys Ser Ser Gly Asp Leu Val Asp Leu Phe Asp Gly Thr Ser Gln Ser
 325 330 335

Thr Gly Gly Ser Ala Asp Leu Phe Gly Gly Phe Ala Asp Phe Gly Ser
 340 345 350

Ala Ala Ala Ser Gly Ser Phe Pro Ser Gln Val Thr Ala Thr Ser Gly
 355 360 365

Asn Gly Asp Phe Gly Asp Trp Ser Ala Phe Asn Gln Ala Pro Ser Gly
 370 375 380

Pro Val Ala Ser Ser Gly Glu Phe Phe Gly Ser Ala Ser Gln Pro Ala
 385 390 395 400

Val Glu Leu Val Ser Gly Ser Gln Ser Ala Leu Gly Pro Pro Pro Ala
 405 410 415

Ala Ser Asn Ser Ser Asp Leu Phe Asp Leu Met Gly Ser Ser Gln Ala
 420 425 430

Thr Met Thr Ser Ser Gln Ser Met Asn Phe Ser Met Met Ser Thr Asn
 435 440 445

Thr Val Gly Leu Gly Leu Pro Met Ser Arg Ser Gln Asn Thr Asp Met
450 455 460

Val Gln Lys Ser Val Ser Lys Thr Leu Pro Ser Thr Trp Ser Asp Pro
465 470 475 480

Ser Val Asn Ile Ser Leu Asp Asn Leu Leu Pro Gly Met Gln Pro Ser
485 490 495

Lys Pro Gln Gln Pro Ser Leu Asn Thr Met Ile Gln Gln Gln Asn Met
500 505 510

Gln Gln Pro Met Asn Val Met Thr Gln Ser Phe Gly Ala Val Asn Leu
515 520 525

Ser Ser Pro Ser Asn Met Leu Pro Val Arg Pro Gln Thr Asn Ala Leu
530 535 540

Ile Gly Gly Pro Met Pro Met Ser Met Pro Asn Val Met Thr Gly Thr
545 550 555 560

Met Gly Met Ala Pro Leu Gly Asn Thr Pro Met Met Asn Gln Ser Met
565 570 575

Met Gly Met Asn Met Asn Ile Gly Met Ser Ala Ala Gly Met Gly Leu
580 585 590

Thr Gly Thr Met Gly Met Gly Met Pro Asn Ile Ala Met Thr Ser Gly
595 600 605

Thr Val Gln Pro Lys Gln Asp Ala Phe Ala Asn Phe Ala Asn Phe Ser
610 615 620

Lys
625

<210> 3

<211> 2705

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> CDS

<222> (262)..(2208)

<223>

<400> 3

ggacacgaca gctcaccaaa tattagctgc tgtgattttg ttttacaatt ttcgttttaa	60
tttttacatt tttgtttgcg gaaagcgcggt gtgagagaca ggtgagccgt ttccatgcaa	120
aagtgcaaat cgtagctgc aaaacagtca gaaaacggca cgccaagcga aaacgagttc	180
gacgtcttgt ttagattgga tttccagcc acttttcgac gagattgtgt gaaaaattcc	240
gtagcattca atagtctcaa a atg gtg gat aaa ttc atc agc atg tgg aaa	291
Met Val Asp Lys Phe Ile Ser Met Trp Lys	
1 5 10	
gtg cgc gaa ttg gcg gac aag gtc acc aat gtc gtg atg aat tac acg	339
Val Arg Glu Leu Ala Asp Lys Val Thr Asn Val Val Met Asn Tyr Thr	
15 20 25	
gaa acg gag ggc aag gtg cgg gag gcc acc aac gat gat cct tgg ggg	387
Glu Thr Glu Gly Lys Val Arg Glu Ala Thr Asn Asp Asp Pro Trp Gly	
30 35 40	
cct aca gga ccc ctc atg cag gaa ttg gcc tat tcc acc ttc tca tac	435
Pro Thr Gly Pro Leu Met Gln Glu Leu Ala Tyr Ser Thr Phe Ser Tyr	
45 50 55	
gaa aca ttc ccg gag gtg atg tcc atg ctg tgg aag cgc atg ctg cag	483
Glu Thr Phe Pro Glu Val Met Ser Met Leu Trp Lys Arg Met Leu Gln	
60 65 70	
gac aat aaa acc aac tgg cga cgc acg tac aag agc ctc ctt ctg cta	531
Asp Asn Lys Thr Asn Trp Arg Arg Thr Tyr Lys Ser Leu Leu Leu Leu	
75 80 85 90	
aac tat ttg gtg cga aac ggc tct gaa cgg gtg gta acc tcc tct cgg	579
Asn Tyr Leu Val Arg Asn Gly Ser Glu Arg Val Val Thr Ser Ser Arg	
95 100 105	
gag cac atc tac gat ctg cgc tcg ctg gag aac tat aca ttc acc gac	627
Glu His Ile Tyr Asp Leu Arg Ser Leu Glu Asn Tyr Thr Phe Thr Asp	
110 115 120	
gag ggc ggc aag gat cag ggt att aat gtt agg cat aag gta cga gag	675
Glu Gly Gly Lys Asp Gln Gly Ile Asn Val Arg His Lys Val Arg Glu	
125 130 135	

ctt ata gac ttt att cag gat gat gat cgt ttg cgc gag gag cgc aaa	723
Leu Ile Asp Phe Ile Gln Asp Asp Arg Leu Arg Glu Glu Arg Lys	
140 145 150	
aag gcg aag aag aac aag gac aag tac atc ggc atg agc agc gac gcc	771
Lys Ala Lys Lys Asn Lys Asp Lys Tyr Ile Gly Met Ser Ser Asp Ala	
155 160 165 170	
atg ggc atg cga agc ggt ggc tac agc ggc tat agc ggt gga tct gga	819
Met Gly Met Arg Ser Gly Gly Tyr Ser Gly Tyr Ser Gly Gly Ser Gly	
175 180 185	
gga ggc ggc ggt ggc agc ggt ggc tac aat gat ggc gac tat cgc tct	867
Gly Gly Gly Gly Gly Ser Gly Gly Tyr Asn Asp Gly Asp Tyr Arg Ser	
190 195 200	
agt cgt gga gac aat tgg tac tcc gac aaa agc gcc gac aag gat cgg	915
Ser Arg Gly Asp Asn Trp Tyr Ser Asp Lys Ser Ala Asp Lys Asp Arg	
205 210 215	
tat gag gat gat gat act cac tac gat gga gag cga gag gga tcc gat	963
Tyr Glu Asp Asp Asp Thr His Tyr Asp Gly Glu Arg Glu Gly Ser Asp	
220 225 230	
agc gac tca ccc agt cca aga cgt aac tat cga tac aat gac cgt gcg	1011
Ser Asp Ser Pro Ser Pro Arg Arg Asn Tyr Arg Tyr Asn Asp Arg Ala	
235 240 245 250	
agt cct gcc gaa gta gcc agc gag gcc aaa cct tcc agc ctc aac atg	1059
Ser Pro Ala Glu Val Ala Ser Glu Ala Lys Pro Ser Ser Leu Asn Met	
255 260 265	
aac att cgt tcg aag acc gtc agt tcc cct gtc tcc aag cag ccc act	1107
Asn Ile Arg Ser Lys Thr Val Ser Ser Pro Val Ser Lys Gln Pro Thr	
270 275 280	
tca acg gct tct gcc aag cca gcg ctg tcc cag aag aag atc gat ctg	1155
Ser Thr Ala Ser Ala Lys Pro Ala Leu Ser Gln Lys Lys Ile Asp Leu	
285 290 295	
ggt gcg gca gca aac ttt gga aag cca gct cct ggc ggt gct gct ggc	1203
Gly Ala Ala Ala Asn Phe Gly Lys Pro Ala Pro Gly Gly Ala Ala Gly	
300 305 310	
att cac tca cca act cac cgt gac act ccc acc agc gtg gac ttg atg	1251
Ile His Ser Pro Thr His Arg Asp Thr Pro Thr Ser Val Asp Leu Met	
315 320 325 330	
ggc ggc gct tcg cca tcg ccg tct act tcc aag gca aac aat aat acg	1299
Gly Gly Ala Ser Pro Ser Pro Ser Thr Ser Lys Ala Asn Asn Asn Thr	
335 340 345	
caa agc aat aac aac gat ctg ctg gac gat ctg ttc aag acc tgc tcg	1347
Gln Ser Asn Asn Asn Asp Leu Leu Asp Asp Leu Phe Lys Thr Cys Ser	

350	355	360	
cca ccg ccg ggg cag gag aag acg ctg aac agt gct gcc gtg att gtg Pro Pro Pro Gly Gln Glu Lys Thr Leu Asn Ser Ala Ala Val Ile Val 365 370 375			1395
gat gac gat gat gac ttc aat ccg cgt gcc agc gat gct agc cag cag Asp Asp Asp Asp Asp Phe Asn Pro Arg Ala Ser Asp Ala Ser Gln Gln 380 385 390			1443
gaa ttc ggc gac ttc gcc tct gct ttc ggg cag ccc tcg gcg gga tcg Glu Phe Gly Asp Phe Ala Ser Ala Phe Gly Gln Pro Ser Ala Gly Ser 395 400 405 410			1491
acg atc agc gag cca cca tca acg ggc ctg gtt ccg gct gcg aac gat Thr Ile Ser Glu Pro Pro Ser Thr Gly Leu Val Pro Ala Ala Asn Asp 415 420 425			1539
gag ttc gcc gac ttt gcg gcg ttc caa ggc tcg aca acg tcg aca tct Glu Phe Ala Asp Phe Ala Ala Phe Gln Gly Ser Thr Thr Ser Thr Ser 430 435 440			1587
gcg ctg gac ggt aat ttg ctg aag act gcc acg ccg gcg aac gat tcg Ala Leu Asp Gly Asn Leu Leu Lys Thr Ala Thr Pro Ala Asn Asp Ser 445 450 455			1635
ttt gac ctg ttt aat tca gct ccc acc tcg acg gca gca gcc aca acg Phe Asp Leu Phe Asn Ser Ala Pro Thr Ser Thr Ala Ala Ala Thr Thr 460 465 470			1683
gct aca gat ctc ctg gca ggc ctg ggc gat ctg tcc att cac caa agc Ala Thr Asp Leu Leu Ala Gly Leu Gly Asp Leu Ser Ile His Gln Ser 475 480 485 490			1731
atg ccc atg gac aat atg atg cct ccc att ccc gcc gtc acg ggc aat Met Pro Met Asp Asn Met Met Pro Pro Ile Pro Ala Val Thr Gly Asn 495 500 505			1779
aat ctg ctc cag ccc atg tcg gtg acc aat aat aac aat aat acc aac Asn Leu Leu Gln Pro Met Ser Val Thr Asn Asn Asn Asn Asn Thr Asn 510 515 520			1827
gga ggc gca gtc ccc gcc gct gcc agt gtc cag tct acc gct gtg ggc Gly Gly Ala Val Pro Ala Ala Ser Val Gln Ser Thr Ala Val Gly 525 530 535			1875
gcc acc tgg tcg ggc gac ctg aag ggc ggc aag atg aac att gac ctg Ala Thr Trp Ser Gly Asp Leu Lys Gly Gly Lys Met Asn Ile Asp Leu 540 545 550			1923
gac aat ctg ctg atg agc aag tcg ggc aag ccc agt gcc ccg gcc cct Asp Asn Leu Leu Met Ser Lys Ser Gly Lys Pro Ser Ala Pro Ala Pro 555 560 565 570			1971
tcg atg aat gcc ctg aag acc aac agt ccg gca aag gcg cca ctg aat			2019

Ser Met Asn Ala Leu Lys Thr Asn Ser Pro Ala Lys Ala Pro Leu Asn	
575 580 585	
gtg cag acg ggt ggc gga ttc cct gga ctg tcg cca atg acc agt ccg	2067
Val Gln Thr Gly Gly Gly Phe Pro Gly Leu Ser Pro Met Thr Ser Pro	
590 595 600	
aac att ttt ggg gct ccg gca ccg cag caa agc att cca caa aac caa	2115
Asn Ile Phe Gly Ala Pro Ala Pro Gln Gln Ser Ile Pro Gln Asn Gln	
605 610 615	
tca gca ttt gcc aac ttt gga gct ttc cag cag cag cag cag aat cac	2163
Ser Ala Phe Ala Asn Phe Gly Ala Phe Gln Gln Gln Gln Gln Asn His	
620 625 630	
agc aat aat aac aat aat agc tcg tcg gca ttc gac ttg ttt caa	2208
Ser Asn Asn Asn Asn Asn Ser Ser Ser Ala Phe Asp Leu Phe Gln	
635 640 645	
tgatattttt tagcctaatt taacccaacc aacctactac ccaaaatgtc cactctcaca	2268
ttcacatttc cagatcgct aaacttggtca gttctatata ttatttacgt tttcctttcc	2328
ccttgctgta caaagtttgc gacacgtgca atttgtttct aaattcgttg ttaaacaatt	2388
tacccccgat gcaattttcc ggatcaaacc cattaattcc acatccgtcc tgatcgcca	2448
ctcggaattt gaaagtcgtc atcaaagtca atacacagag tagttgaata atggttgtac	2508
taaacggatt cgtagcaca acgcgcggac ggacggctga gcgatccaac attgaaattg	2568
ttaaacaaaa tactacacgt aataaaatca aacaatttta gcaatagtta acgttacgat	2628
gtgtctgtat ataaattgaa tgtaaagcaa atatgaaata taaaacaatt gaaaccaata	2688
aaaaaaaaaa aaaaaaa	2705

<210> 4

<211> 649

<212> PRT

<213> Drosophila melanogaster

<400> 4

Met Val Asp Lys Phe Ile Ser Met Trp Lys Val Arg Glu Leu Ala Asp
1 5 10 15
Lys Val Thr Asn Val Val Met Asn Tyr Thr Glu Thr Glu Gly Lys Val
20 25 30

Arg Glu Ala Thr Asn Asp Asp Pro Trp Gly Pro Thr Gly Pro Leu Met
35 40 45

Gln Glu Leu Ala Tyr Ser Thr Phe Ser Tyr Glu Thr Phe Pro Glu Val
50 55 60

Met Ser Met Leu Trp Lys Arg Met Leu Gln Asp Asn Lys Thr Asn Trp
65 70 75 80

Arg Arg Thr Tyr Lys Ser Leu Leu Leu Leu Asn Tyr Leu Val Arg Asn
85 90 95

Gly Ser Glu Arg Val Val Thr Ser Ser Arg Glu His Ile Tyr Asp Leu
100 105 110

Arg Ser Leu Glu Asn Tyr Thr Phe Thr Asp Glu Gly Gly Lys Asp Gln
115 120 125

Gly Ile Asn Val Arg His Lys Val Arg Glu Leu Ile Asp Phe Ile Gln
130 135 140

Asp Asp Asp Arg Leu Arg Glu Glu Arg Lys Lys Ala Lys Lys Asn Lys
145 150 155 160

Asp Lys Tyr Ile Gly Met Ser Ser Asp Ala Met Gly Met Arg Ser Gly
165 170 175

Gly Tyr Ser Gly Tyr Ser Gly Gly Ser Gly Gly Gly Gly Gly Ser
180 185 190

Gly Gly Tyr Asn Asp Gly Asp Tyr Arg Ser Ser Arg Gly Asp Asn Trp
195 200 205

Tyr Ser Asp Lys Ser Ala Asp Lys Asp Arg Tyr Glu Asp Asp Asp Thr
210 215 220

His Tyr Asp Gly Glu Arg Glu Gly Ser Asp Ser Asp Ser Pro Ser Pro
225 230 235 240

Arg Arg Asn Tyr Arg Tyr Asn Asp Arg Ala Ser Pro Ala Glu Val Ala
245 250 255

Ser Glu Ala Lys Pro Ser Ser Leu Asn Met Asn Ile Arg Ser Lys Thr
260 265 270

Val Ser Ser Pro Val Ser Lys Gln Pro Thr Ser Thr Ala Ser Ala Lys
275 280 285

Pro Ala Leu Ser Gln Lys Lys Ile Asp Leu Gly Ala Ala Ala Asn Phe
290 295 300

Gly Lys Pro Ala Pro Gly Gly Ala Ala Gly Ile His Ser Pro Thr His
305 310 315 320

Arg Asp Thr Pro Thr Ser Val Asp Leu Met Gly Gly Ala Ser Pro Ser
325 330 335

Pro Ser Thr Ser Lys Ala Asn Asn Asn Thr Gln Ser Asn Asn Asn Asp
340 345 350

Leu Leu Asp Asp Leu Phe Lys Thr Cys Ser Pro Pro Pro Gly Gln Glu
355 360 365

Lys Thr Leu Asn Ser Ala Ala Val Ile Val Asp Asp Asp Asp Phe
370 375 380

Asn Pro Arg Ala Ser Asp Ala Ser Gln Gln Glu Phe Gly Asp Phe Ala
385 390 395 400

Ser Ala Phe Gly Gln Pro Ser Ala Gly Ser Thr Ile Ser Glu Pro Pro
405 410 415

Ser Thr Gly Leu Val Pro Ala Ala Asn Asp Glu Phe Ala Asp Phe Ala
420 425 430

Ala Phe Gln Gly Ser Thr Thr Ser Thr Ser Ala Leu Asp Gly Asn Leu
435 440 445

Leu Lys Thr Ala Thr Pro Ala Asn Asp Ser Phe Asp Leu Phe Asn Ser
450 455 460

Ala Pro Thr Ser Thr Ala Ala Ala Thr Thr Ala Thr Asp Leu Leu Ala
465 470 475 480

Gly Leu Gly Asp Leu Ser Ile His Gln Ser Met Pro Met Asp Asn Met

485

490

495

Met Pro Pro Ile Pro Ala Val Thr Gly Asn Asn Leu Leu Gln Pro Met
 500 505 510

Ser Val Thr Asn Asn Asn Asn Asn Thr Asn Gly Gly Ala Val Pro Ala
 515 520 525

Ala Ala Ser Val Gln Ser Thr Ala Val Gly Ala Thr Trp Ser Gly Asp
 530 535 540

Leu Lys Gly Gly Lys Met Asn Ile Asp Leu Asp Asn Leu Leu Met Ser
 545 550 555 560

Lys Ser Gly Lys Pro Ser Ala Pro Ala Pro Ser Met Asn Ala Leu Lys
 565 570 575

Thr Asn Ser Pro Ala Lys Ala Pro Leu Asn Val Gln Thr Gly Gly Gly
 580 585 590

Phe Pro Gly Leu Ser Pro Met Thr Ser Pro Asn Ile Phe Gly Ala Pro
 595 600 605

Ala Pro Gln Gln Ser Ile Pro Gln Asn Gln Ser Ala Phe Ala Asn Phe
 610 615 620

Gly Ala Phe Gln Gln Gln Gln Asn His Ser Asn Asn Asn Asn Asn
 625 630 635 640

Ser Ser Ser Ala Phe Asp Leu Phe Gln
 645

<210> 5

<211> 643

<212> PRT

<213> Homo sapiens

<400> 5

Met Leu Asn Met Trp Lys Val Arg Glu Leu Val Asp Lys Ala Thr Asn
 1 5 10 15

Val Val Met Asn Tyr Ser Glu Ile Glu Ser Lys Val Arg Glu Ala Thr
20 25 30

Asn Asp Asp Pro Trp Gly Pro Ser Gly Gln Leu Met Gly Glu Ile Ala
35 40 45

Lys Ala Thr Phe Met Tyr Glu Gln Phe Pro Glu Leu Met Asn Met Leu
50 55 60

Trp Ser Arg Met Leu Lys Asp Asn Lys Lys Asn Trp Arg Arg Val Tyr
65 70 75 80

Lys Ser Leu Leu Leu Leu Ala Tyr Leu Ile Arg Asn Gly Ser Glu Arg
85 90 95

Val Val Thr Ser Ala Arg Glu His Ile Tyr Asp Leu Arg Ser Leu Glu
100 105 110

Asn Tyr His Phe Val Asp Glu His Gly Lys Asp Gln Gly Ile Asn Ile
115 120 125

Arg Gln Lys Val Lys Glu Leu Val Glu Phe Ala Gln Asp Asp Asp Arg
130 135 140

Leu Arg Glu Glu Arg Lys Lys Ala Lys Lys Asn Lys Asp Lys Tyr Val
145 150 155 160

Gly Val Ser Ser Asp Ser Val Gly Gly Phe Arg Tyr Ser Glu Arg Tyr
165 170 175

Asp Pro Glu Pro Lys Ser Lys Trp Asp Glu Glu Trp Asp Lys Asn Lys
180 185 190

Ser Ala Phe Pro Phe Ser Asp Lys Leu Gly Glu Leu Ser Asp Lys Ile
195 200 205

Gly Ser Thr Ile Asp Asp Thr Ile Ser Lys Phe Arg Arg Lys Asp Arg
210 215 220

Glu Asp Ser Pro Glu Arg Cys Ser Asp Ser Asp Glu Glu Lys Lys Ala
225 230 235 240

Arg Arg Gly Arg Ser Pro Lys Gly Glu Phe Lys Asp Glu Glu Glu Thr
245 250 255

Val Thr Thr Lys His Ile His Ile Thr Gln Ala Thr Glu Thr Thr Thr
260 265 270

Thr Arg His Lys Arg Thr Ala Asn Pro Ser Lys Thr Ile Asp Leu Gly
275 280 285

Ala Ala Ala His Tyr Thr Gly Asp Lys Ala Ser Pro Asp Gln Asn Ala
290 295 300

Ser Thr His Thr Pro Gln Ser Ser Val Lys Thr Ser Val Pro Ser Ser
305 310 315 320

Lys Ser Ser Gly Asp Leu Val Asp Leu Phe Asp Gly Thr Ser Gln Ser
325 330 335

Thr Gly Gly Ser Ala Asp Leu Phe Gly Gly Phe Ala Asp Phe Gly Ser
340 345 350

Ala Ala Ala Ser Gly Ser Phe Pro Ser Gln Val Thr Ala Thr Ser Gly
355 360 365

Asn Gly Asp Phe Gly Asp Trp Ser Ala Phe Asn Gln Ala Pro Ser Gly
370 375 380

Pro Val Ala Ser Ser Gly Glu Phe Phe Gly Ser Ala Ser Gln Pro Ala
385 390 395 400

Val Glu Leu Val Ser Gly Ser Gln Ser Ala Leu Gly Pro Pro Pro Ala
405 410 415

Ala Ser Asn Ser Ser Asp Leu Phe Asp Leu Met Gly Ser Ser Gln Ala
420 425 430

Thr Met Thr Ser Ser Gln Ser Met Asn Phe Ser Met Met Ser Thr Asn
435 440 445

Thr Val Gly Leu Gly Leu Pro Met Ser Arg Ser Gln Pro Leu Gln Asn
450 455 460

Val Ser Thr Val Leu Gln Lys Pro Asn Pro Leu Tyr Asn Gln Asn Thr
465 470 475 480

Asp Met Val Gln Lys Ser Val Ser Lys Thr Leu Pro Ser Thr Trp Ser
485 490 495

Asp Pro Ser Val Asn Ile Ser Leu Asp Asn Leu Leu Pro Gly Met Gln
500 505 510

Pro Ser Lys Pro Gln Gln Pro Ser Leu Asn Thr Met Ile Gln Gln Gln
515 520 525

Asn Met Gln Gln Pro Met Asn Val Met Thr Gln Ser Phe Gly Ala Val
530 535 540

Asn Leu Ser Ser Pro Ser Asn Met Leu Pro Val Arg Pro Gln Thr Asn
545 550 555 560

Ala Leu Ile Gly Gly Pro Met Pro Met Ser Met Pro Asn Val Met Thr
565 570 575

Gly Thr Met Gly Met Ala Pro Leu Gly Asn Thr Pro Met Met Asn Gln
580 585 590

Ser Met Met Gly Met Asn Met Asn Ile Gly Met Ser Ala Ala Gly Met
595 600 605

Gly Leu Thr Gly Thr Met Gly Met Gly Met Pro Asn Ile Ala Met Thr
610 615 620

Ser Gly Thr Val Gln Pro Lys Gln Asp Ala Phe Ala Asn Phe Ala Asn
625 630 635 640

Phe Ser Lys